

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/565,020
Source: IFWP
Date Processed by STIC: 1-27-06

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IFWP

RAW SEQUENCE LISTING

DATE: 01/27/2006

PATENT APPLICATION: US/10/565,020

TIME: 10:01:12

Input Set : F:\PR60235USw SEQ LIST.txt

Output Set: N:\CRF4\01272006\J565020.raw

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4 <110> APPLICANT: SmithKline Beecham Corporation
5      Lambert, Millard H
6      Xu, Robert
7      Wisely , Bruce
8      Collins, Jon
10 <120> TITLE OF INVENTION: CAR LIGAND-BINDING DOMAIN POLYPEPTIDE CO-CRYSTALLIZED WITH A
11      LIGAND, AND METHODS OF DESIGNING LIGANDS THAT MODULATE CAR
12      ACTIVITY
14 <130> FILE REFERENCE: PR60235
C--> 16 <140> CURRENT APPLICATION NUMBER: US/10/565,020
C--> 16 <141> CURRENT FILING DATE: 2006-01-18
16 <150> PRIOR APPLICATION NUMBER: 60/488,415
17 <151> PRIOR FILING DATE: 2003-07-18
19 <160> NUMBER OF SEQ ID NOS: 7
21 <170> SOFTWARE: PatentIn version 3.2
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 1450
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (273)..(1316)
32 <400> SEQUENCE: 1
33 gtgagcttgc tccttaagtt acaggaactc tccttataat agacacttca ttttcctagt      60
35 ccatacctca tgaaaaatga ctgaccactg ctgggcagca ggagggatga taatcctaac      120
37 tccaatcact ggcaactcct gagatcagag gaaaaccagc aacagcgtgg gagtttgggg      180
39 agaggcattc cataccagat tctgtggcct gcaggtgaca tgctgcctaa gagaagcagg      240
41 agtctgtgac agccaccca acacgtgacg tc atg gcc agt agg gaa gat gag      293
42                                     Met Ala Ser Arg Glu Asp Glu
43                                     1           5
45 ctg agg aac tgt gtg gta tgt ggg gac caa gcc aca ggc tac cac ttt      341
46 Leu Arg Asn Cys Val Val Cys Gly Asp Gln Ala Thr Gly Tyr His Phe
47      10           15           20
49 aat gcg ctg act tgt gag ggc tgc aag ggt ttc ttc agg aga aca gtc      389
50 Asn Ala Leu Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Thr Val
51      25           30           35
53 agc aaa agc att ggt ccc acc tgc ccc ttt gct gga agc tgt gaa gtc      437
54 Ser Lys Ser Ile Gly Pro Thr Cys Pro Phe Ala Gly Ser Cys Glu Val
55 40           45           50           55
57 agc aag act cag agg cgc cac tgc cca gcc tgc agg ttg cag aag tgc      485
58 Ser Lys Thr Gln Arg Arg His Cys Pro Ala Cys Arg Leu Gln Lys Cys
59      60           65           70
61 tta gat gct ggc atg agg aaa gac atg ata ctg tcg gca gaa gcc ctg      533

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62 Leu Asp Ala Gly Met Arg Lys Asp Met Ile Leu Ser Ala Glu Ala Leu
63          75          80          85
65 gca ttg cgg cga gca aag cag gcc cag cgg cgg gca cag caa aca cct      581
66 Ala Leu Arg Arg Ala Lys Gln Ala Gln Arg Arg Ala Gln Gln Thr Pro
67          90          95          100
68 gtg caa ctg agt aag gag caa gaa gag ctg atc cgg aca ctc ctg ggg      629
69 Val Gln Leu Ser Lys Glu Gln Glu Glu Leu Ile Arg Thr Leu Leu Gly
70          105          110          115
73 gcc cac acc cgc cac atg ggc acc atg ttt gaa cag ttt gtg cag ttt      677
74 Ala His Thr Arg His Met Gly Thr Met Phe Glu Gln Phe Val Gln Phe
75 120          125          130          135
77 agg cct cca gct cat ctg ttc atc cat cac cag ccc ttg ccc acc ctg      725
78 Arg Pro Pro Ala His Leu Phe Ile His His Gln Pro Leu Pro Thr Leu
79          140          145          150
81 gcc cct gtg ctg cct ctg gtc aca cac ttc gca gac atc aac act ttc      773
82 Ala Pro Val Leu Pro Leu Val Thr His Phe Ala Asp Ile Asn Thr Phe
83          155          160          165
85 atg gta ctg caa gtc atc aag ttt act aag gac ctg ccc gtc ttc cgt      821
86 Met Val Leu Gln Val Ile Lys Phe Thr Lys Asp Leu Pro Val Phe Arg
87          170          175          180
89 tcc ctg ccc att gaa gac cag atc tcc ctt ctc aag gga gca gct gtg      869
90 Ser Leu Pro Ile Glu Asp Gln Ile Ser Leu Leu Lys Gly Ala Ala Val
91          185          190          195
93 gaa atc tgt cac atc gta ctc aat acc act ttc tgt ctc caa aca caa      917
94 Glu Ile Cys His Ile Val Leu Asn Thr Thr Phe Cys Leu Gln Thr Gln
95 200          205          210          215
97 aac ttc ctc tgc ggg cct ctt cgc tac aca att gaa gat gga gcc cgt      965
98 Asn Phe Leu Cys Gly Pro Leu Arg Tyr Thr Ile Glu Asp Gly Ala Arg
99          220          225          230
101 gtg ggg ttc cag gta gag ttt ttg gag ttg ctc ttt cac ttc cat gga      1013
102 Val Gly Phe Gln Val Glu Phe Leu Glu Leu Leu Phe His Phe His Gly
103          235          240          245
105 aca cta cga aaa ctg cag ctc caa gag cct gag tat gtg ctc ttg gct      1061
106 Thr Leu Arg Lys Leu Gln Leu Gln Glu Pro Glu Tyr Val Leu Leu Ala
107          250          255          260
109 gcc atg gcc ctc ttc tct cct gac cga cct gga gtt acc cag aga gat      1109
110 Ala Met Ala Leu Phe Ser Pro Asp Arg Pro Gly Val Thr Gln Arg Asp
111          265          270          275
113 gag att gat cag ctg caa gag gag atg gca ctg act ctg caa agc tac      1157
114 Glu Ile Asp Gln Leu Gln Glu Glu Met Ala Leu Thr Leu Gln Ser Tyr
115 280          285          290          295
117 atc aag ggc cag cag cga agg ccc cgg gat cgg ttt ctg tat gcg aag      1205
118 Ile Lys Gly Gln Gln Arg Arg Pro Arg Asp Arg Phe Leu Tyr Ala Lys
119          300          305          310
121 ttg cta ggc ctg ctg gct gag ctc cgg agc att aat gag gcc tac ggg      1253
122 Leu Leu Gly Leu Leu Ala Glu Leu Arg Ser Ile Asn Glu Ala Tyr Gly
123          315          320          325
125 tac caa atc cag cac atc cag ggc ctg tct gcc atg atg ccg ctg ctc      1301
126 Tyr Gln Ile Gln His Ile Gln Gly Leu Ser Ala Met Met Pro Leu Leu

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127          330          335          340
129 cag gag atc tgc agc tgaggccatg ctcaattcct tccccagctc acctggaaca      1356
130 Gln Glu Ile Cys Ser
131          345
133 ccctggatac actggagtgg gaaaatgctg ggaccaaaga ttggggccggg ttcaaaggga      1416
135 gcccagtggg tgcaatgaaa gactaaagca aaac                                1450
141 <210> SEQ ID NO: 2
142 <211> LENGTH: 348
143 <212> TYPE: PRT
144 <213> ORGANISM: Homo sapiens
146 <400> SEQUENCE: 2
148 Met Ala Ser Arg Glu Asp Glu Leu Arg Asn Cys Val Val Cys Gly Asp
149 1          5          10          15
151 Gln Ala Thr Gly Tyr His Phe Asn Ala Leu Thr Cys Glu Gly Cys Lys
152          20          25          30
154 Gly Phe Phe Arg Arg Thr Val Ser Lys Ser Ile Gly Pro Thr Cys Pro
155          35          40          45
157 Phe Ala Gly Ser Cys Glu Val Ser Lys Thr Gln Arg Arg His Cys Pro
158          50          55          60
160 Ala Cys Arg Leu Gln Lys Cys Leu Asp Ala Gly Met Arg Lys Asp Met
161 65          70          75          80
163 Ile Leu Ser Ala Glu Ala Leu Ala Leu Arg Arg Ala Lys Gln Ala Gln
164          85          90          95
166 Arg Arg Ala Gln Gln Thr Pro Val Gln Leu Ser Lys Glu Gln Glu Glu
167          100         105         110
169 Leu Ile Arg Thr Leu Leu Gly Ala His Thr Arg His Met Gly Thr Met
170          115         120         125
172 Phe Glu Gln Phe Val Gln Phe Arg Pro Pro Ala His Leu Phe Ile His
173          130         135         140
175 His Gln Pro Leu Pro Thr Leu Ala Pro Val Leu Pro Leu Val Thr His
176 145         150         155         160
178 Phe Ala Asp Ile Asn Thr Phe Met Val Leu Gln Val Ile Lys Phe Thr
179          165         170         175
181 Lys Asp Leu Pro Val Phe Arg Ser Leu Pro Ile Glu Asp Gln Ile Ser
182          180         185         190
184 Leu Leu Lys Gly Ala Ala Val Glu Ile Cys His Ile Val Leu Asn Thr
185          195         200         205
187 Thr Phe Cys Leu Gln Thr Gln Asn Phe Leu Cys Gly Pro Leu Arg Tyr
188          210         215         220
190 Thr Ile Glu Asp Gly Ala Arg Val Gly Phe Gln Val Glu Phe Leu Glu
191 225         230         235         240
194 Leu Leu Phe His Phe His Gly Thr Leu Arg Lys Leu Gln Leu Gln Glu
195          245         250         255
197 Pro Glu Tyr Val Leu Leu Ala Ala Met Ala Leu Phe Ser Pro Asp Arg
198          260         265         270
200 Pro Gly Val Thr Gln Arg Asp Glu Ile Asp Gln Leu Gln Glu Glu Met
201          275         280         285
203 Ala Leu Thr Leu Gln Ser Tyr Ile Lys Gly Gln Gln Arg Arg Pro Arg
204          290         295         300

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206 Asp Arg Phe Leu Tyr Ala Lys Leu Leu Gly Leu Leu Ala Glu Leu Arg
207 305          310          315          320
209 Ser Ile Asn Glu Ala Tyr Gly Tyr Gln Ile Gln His Ile Gln Gly Leu
210          325          330          335
212 Ser Ala Met Met Pro Leu Leu Gln Glu Ile Cys Ser
213          340          345
215 <210> SEQ ID NO: 3
216 <211> LENGTH: 714
217 <212> TYPE: DNA
218 <213> ORGANISM: Homo sapiens
220 <220> FEATURE:
221 <221> NAME/KEY: CDS
222 <222> LOCATION: (1)..(714)
224 <400> SEQUENCE: 3
225 cct gtg caa ctg agt aag gag caa gaa gag ctg atc cgg aca ctc ctg      48
226 Pro Val Gln Leu Ser Lys Glu Gln Glu Glu Leu Ile Arg Thr Leu Leu
227 1          5          10          15
229 ggg gcc cac acc cgc cac atg ggc acc atg ttt gaa cag ttt gtg cag      96
230 Gly Ala His Thr Arg His Met Gly Thr Met Phe Glu Gln Phe Val Gln
231          20          25          30
233 ttt agg cct cca gct cat ctg ttc atc cat cac cag ccc ttg ccc acc      144
234 Phe Arg Pro Pro Ala His Leu Phe Ile His His Gln Pro Leu Pro Thr
235          35          40          45
237 ctg gcc cct gtg ctg cct ctg gtc aca cac ttc gca gac atc aac act      192
238 Leu Ala Pro Val Leu Pro Leu Val Thr His Phe Ala Asp Ile Asn Thr
239          50          55          60
241 ttc atg gta ctg caa gtc atc aag ttt act aag gac ctg ccc gtc ttc      240
242 Phe Met Val Leu Gln Val Ile Lys Phe Thr Lys Asp Leu Pro Val Phe
243 65          70          75          80
245 cgt tcc ctg ccc att gaa gac cag atc tcc ctt ctc aag gga gca gct      288
246 Arg Ser Leu Pro Ile Glu Asp Gln Ile Ser Leu Leu Lys Gly Ala Ala
247          85          90          95
249 gtg gaa atc tgt cac atc gta ctc aat acc act ttc tgt ctc caa aca      336
250 Val Glu Ile Cys His Ile Val Leu Asn Thr Thr Phe Cys Leu Gln Thr
251          100          105          110
253 caa aac ttc ctc tgc ggg cct ctt cgc tac aca att gaa gat gga gcc      384
254 Gln Asn Phe Leu Cys Gly Pro Leu Arg Tyr Thr Ile Glu Asp Gly Ala
255          115          120          125
257 cgt gtg ggg ttc cag gta gag ttt ttg gag ttg ctc ttt cac ttc cat      432
258 Arg Val Gly Phe Gln Val Glu Phe Leu Glu Leu Leu Phe His Phe His
259          130          135          140
261 gga aca cta cga aaa ctg cag ctc caa gag cct gag tat gtg ctc ttg      480
262 Gly Thr Leu Arg Lys Leu Gln Leu Gln Glu Pro Glu Tyr Val Leu Leu
263 145          150          155          160
265 gct gcc atg gcc ctc ttc tct cct gac cga cct gga gtt acc cag aga      528
266 Ala Ala Met Ala Leu Phe Ser Pro Asp Arg Pro Gly Val Thr Gln Arg
267          165          170          175
269 gat gag att gat cag ctg caa gag gag atg gca ctg act ctg caa agc      576
270 Asp Glu Ile Asp Gln Leu Gln Glu Glu Met Ala Leu Thr Leu Gln Ser

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271          180          185          190
273 tac atc aag ggc cag cag cga agg ccc cgg gat cgg ttt ctg tat gcg      624
274 Tyr Ile Lys Gly Gln Gln Arg Arg Pro Arg Asp Arg Phe Leu Tyr Ala
275          195          200          205
277 aag ttg cta ggc ctg ctg gct gag ctc cgg agc att aat gag gcc tac      672
278 Lys Leu Leu Gly Leu Leu Ala Glu Leu Arg Ser Ile Asn Glu Ala Tyr
279          210          215          220
281 ggg tac caa atc cag cac atc cag ggc ctg tct gcc atg atg      714
282 Gly Tyr Gln Ile Gln His Ile Gln Gly Leu Ser Ala Met Met
283 225          230          235
285 <210> SEQ ID NO: 4
286 <211> LENGTH: 238
287 <212> TYPE: PRT
288 <213> ORGANISM: Homo sapiens
290 <400> SEQUENCE: 4
292 Pro Val Gln Leu Ser Lys Glu Gln Glu Glu Leu Ile Arg Thr Leu Leu
293 1          5          10          15
295 Gly Ala His Thr Arg His Met Gly Thr Met Phe Glu Gln Phe Val Gln
296          20          25          30
298 Phe Arg Pro Pro Ala His Leu Phe Ile His His Gln Pro Leu Pro Thr
299          35          40          45
301 Leu Ala Pro Val Leu Pro Leu Val Thr His Phe Ala Asp Ile Asn Thr
302          50          55          60
304 Phe Met Val Leu Gln Val Ile Lys Phe Thr Lys Asp Leu Pro Val Phe
305 65          70          75          80
307 Arg Ser Leu Pro Ile Glu Asp Gln Ile Ser Leu Leu Lys Gly Ala Ala
308          85          90          95
310 Val Glu Ile Cys His Ile Val Leu Asn Thr Thr Phe Cys Leu Gln Thr
311          100          105          110
313 Gln Asn Phe Leu Cys Gly Pro Leu Arg Tyr Thr Ile Glu Asp Gly Ala
314          115          120          125
316 Arg Val Gly Phe Gln Val Glu Phe Leu Glu Leu Leu Phe His Phe His
317          130          135          140
319 Gly Thr Leu Arg Lys Leu Gln Leu Gln Glu Pro Glu Tyr Val Leu Leu
320 145          150          155          160
322 Ala Ala Met Ala Leu Phe Ser Pro Asp Arg Pro Gly Val Thr Gln Arg
323          165          170          175
325 Asp Glu Ile Asp Gln Leu Gln Glu Glu Met Ala Leu Thr Leu Gln Ser
326          180          185          190
328 Tyr Ile Lys Gly Gln Gln Arg Arg Pro Arg Asp Arg Phe Leu Tyr Ala
329          195          200          205
331 Lys Leu Leu Gly Leu Leu Ala Glu Leu Arg Ser Ile Asn Glu Ala Tyr
332          210          215          220
334 Gly Tyr Gln Ile Gln His Ile Gln Gly Leu Ser Ala Met Met
335 225          230          235
338 <210> SEQ ID NO: 5
339 <211> LENGTH: 11
340 <212> TYPE: PRT
341 <213> ORGANISM: Artificial

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/565,020

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Input Set : F:\PR60235USw SEQ LIST.txt
Output Set: N:\CRF4\01272006\J565020.raw

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5,6,7 ,

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/565,020

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Input Set : F:\PR60235USw SEQ LIST.txt

Output Set: N:\CRF4\01272006\J565020.raw

L:16 M:270 C: Current Application Number differs, Replaced Current Application No

L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date